

10 30 50 70
 gaattccggcgogtggggcgctgacaggggactcggggggactcttgccagagacccctggaccacgccgccatcgagccctccag
 90 110 130 150 170
 cccogtccctctctgcgcgttctctcctgccatggggcgccgacccgctcggggcttcggagcagcgaccgggcccgggct
 190 210 230 250
 gaccccatgtggcgagagcccggctcctggggcgagctgccgtgcgctccccgggtccgcccccgccgggctcgggt
 270 290 310 330
 cagcatggattcctgggttcattcttgctctgttgccagtggtcctaatcatgttagtgccacccatgctactacagtttcacc
 350 370 390 410
 M D S W F I L V L F G S G L I H V S A N N A T T V S P
 430 450 470 490
 ttctttgggaacgacagatttaattaaacatccaacacgaattggctaaagagagatooaacctcaaatltcaacctcttc
 S L G T T R L I K T S T T E L A K E E N K T S N S T S S
 510 530 550 570 590
 aglaatttctcttctglgccaccacattcagcccaacctgactctggggccacactatgtgactactgttaattcttcaca
 V I S L S V A P T F S P N L T L E P T Y V T T V N S S H
 610 630 650 670
 ctctgacaatgggaccgagggcgccgacgggaatctlggggcactaccatttccccgaacgggaagctggcttattgagaa
 S D N G T R R A A S T E S G G T T I S P N G S W L I E N
 690 710 730 750
 ccagttcacggatgccatocagacccctgggggggaactccagcactgcagcaaccacccagaaaacttccccccggcaga
 Q F T D A I T E P W E G N S S T A A T T P E T F P P A D
 770 790 810 830
 tgagacaccatttctgcggtgatggggccctgctctctctgctgtagtactgttttattatcatogttctgtacatgttaog
 E T P I I A V M V A L S S L L V I V F I I I V L Y M L R
 850 870 890 910
 gtttaagaaatocagcaagctgggggtcatttccaactcttccgcctgtcaaatggccgcacggaggatgtggggcccccgaag
 F K K Y K Q A G S H S N S F R L S N G R T E D V E P Q S

FIG.1A

850 870 880 890 910
 tglccaccltctggccaggtcccgggcccacccagggaggtaccacccactgcctgtggacaagctggagggaggtatcccg
 V P L L A R S P S T N R K Y P P L P V D K L E E I N R
 930 950 970 990 1010
 gggatggctgatgacaatgaagctcttcagggaggaatcaacgctccctgcttctctatccaggccaccltgtgggctgc
 R M A D D N K L F R E E F N A L P A C P I Q A T C E A A
 1030 1050 1070 1090
 clccagggaagaaacccgggaaacccgctatgttaacatcctgcctatgaccactctgagtgaccctgacacclgttg
 S K E E N K E [K N R Y V N I L P Y D H S R V H L T P V E
 1110 1130 1150 1170
 oagggtcccagattctgattacatcaacgcttcattcatttaattggtaccaggaaagaaacaaattcctcgctgcacaaggac
 G V P D S D Y I N A S F I N G Y Q E K N K F I A A Q G P
 1190 1210 1230 1250
 caaagggaagaaacagtgaaatgacttctggaggaatgatatgggaacaaacacagctactatgtcatggtgaccaccltgaagg
 K E E T V N D F W R M I W E Q N T A T I V M V T N L K E
 1270 1290 1310 1330
 agggaaaggagtgtaaatgtgcccaactctggccagaccaggtgctggacctatgggaatgtccgtgtgtctgtcgaggatg
 R K E C K C A Q Y W P D Q G C W T Y G N V R V S V E D V
 1350 1370 1390 1410 1430
 tgactgttctgtggactacacagtcacggaaattctcgatccagcagggtggcgagtgaccacacaggaaacacacagcctcat
 T V L V D Y T V R K F S I Q Q V G D V T N R K P Q R L I
 1450 1470 1490 1510
 caatcagltccacttcaccagctggccagacttgggggtgccttcccccacttgcatgctcaagltccatcaaggagtgag
 T Q F H F T S W P D F G V P F T P I G M L K F L K K V K
 1530 1550 1570 1590
 gactgtacccclcagtcagcggggtatctgtgltccactgcagtgccaggtgagggcgacatggccacttgtgtcatcagtg
 A C N P Q Y A G A I V V H C S A G V G R T G T F V V I D A

FIG.1B

1610 1630 1650 1670
 ccatgctggacatgatgcattcggagcgcaaatggtgtatctatgggtttgtgagccggatccggcccgctgccagatggta
 M L D M M H S E R K V D V Y G F V S R I R A Q R C Q M V
 1690 1710 1730 1750 1770
 cagacagacatgcagtcagtcctcatataccaggccctctggagcattatctgtatggggacacagaaclggaaagtgactctc
 Q T D M Q Y V F I Y] Q A L L E H Y L Y G D T E L E V T S L
 1790 1810 1830 1850
 / tagaaacccacctacaaaaatttatooaagatcccaggacatgcaacacgggttagaggagggtltaagaaatttaacttc
 E T H L Q K I Y N K I P G T S N N G L E E F K K L T S
 1870 1890 1910 1930
 oatlcaaatccagaatgacaagatgcgcacgggaaactccagccaacatgaagaaacgggtttacagatcattccatct
 I K I Q N D K M R T G N L P A N M K [K N R V L Q I I P Y
 1950 1970 1990 2010
 gaatttaacagagtgatcattccagtcacacggagggaggaagacacagactatgtgaacgcatccttcattgatggataccggc
 E F N R V I I P V K R G E E N T D Y V N A S F I D G Y R Q
 2030 2050 2070 2090 2110
 agaaagactcctacattgccagccaggccctctctccacacgattgaggactctggcgaatgatctggaggatggaaagtcctg
 K D S Y I A S Q G P L L H T I E D F W R M I W E W K S C
 2130 2150 2170 2190
 ttctatcgttaatgctgacagaaclggaagagagggccaggaagtggtgccagtlactggccatctgatggcctgggtgctctac
 S I V M L T E L E E R G Q E K C A Q Y W P S D G L V S Y
 2210 2230 2250 2270
 ggagacatcacagttgagctgaagaaagggaggaatgtgaagactacactgtccgagacctcctggtcaccaaccacgggaga II
 G D I T V E L K K E E E C E S Y T V R D L L V T N T R E N

FIG.1C

0.1 kb
1

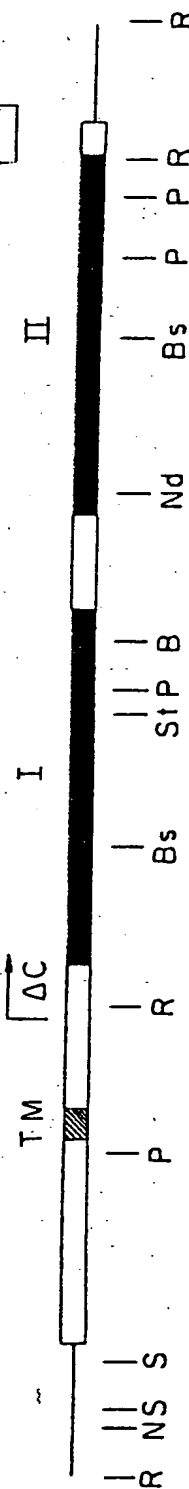


FIG. 1

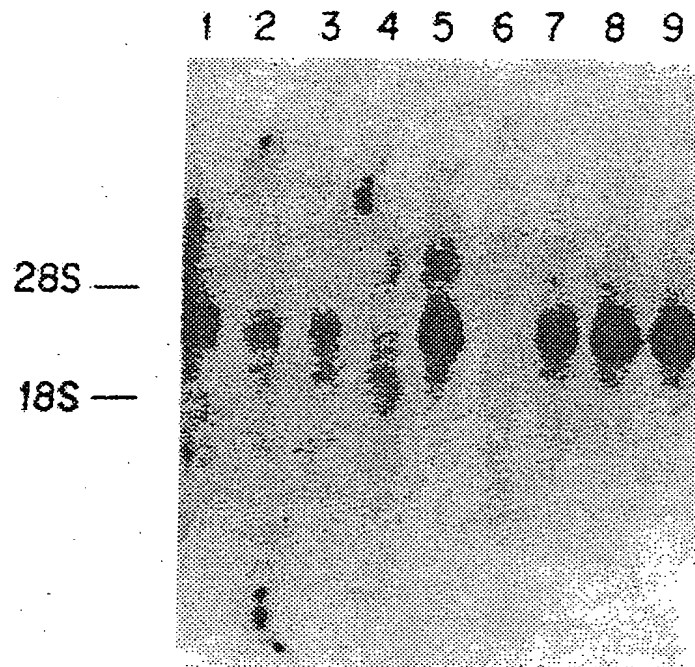


FIG. 2

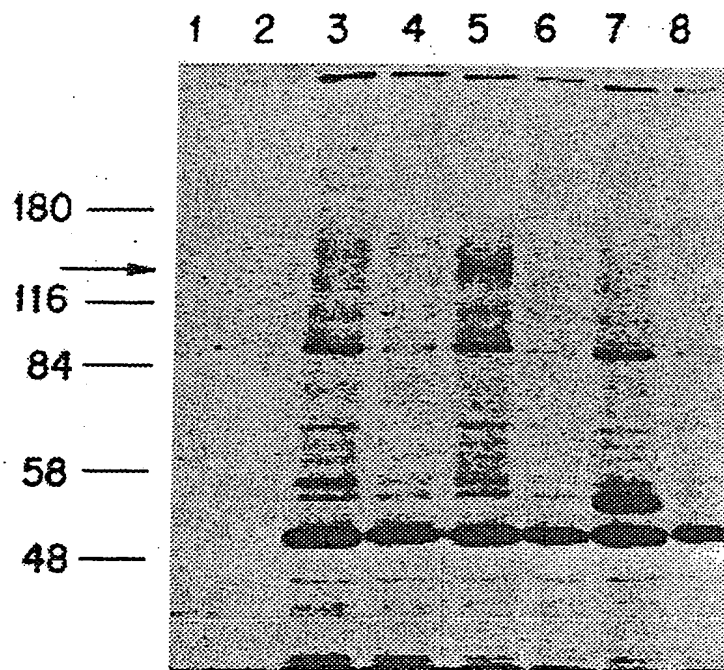


FIG. 3

31-4

27-1

3

Diagram illustrating the structure of poly(2-vinylpyridine) (PVP) showing the sequence of units (I, II, III, IV, V, VI, VII, VIII) and the terminal groups (NH₂ and COOH).

①
1 MDSWF ILVLLGSLICVS ANNATTVAPSVG ITRLINSSTAEPVKEEAKTSNPTSSLTSLSVAPTFFSP 68
2 F H S L T K T L A N S V I 68
1 NITLGPYLTITVNSSDSNGTTRTASINSIGITISPNGTLPDQNFIDARTEPWEGNSSTAATTPETFP 136
2 L E V H R A E G T S I E I 136
1 PSGNSDSKORRDETPIIAAMVALSSLLVIVFIIIVLYMLRFKKYKQAGSHSNFRLSNGRTEDVEPQS 204
2 A 195
1 VPLLARSPSTNRKYPPLPVDKLEEEINRRMADDNKLFREEFNALPACP IQATCEAAASKEENKEKNRYV 272
2 263
1 NILPYDHSRVHLPVEGVPDSYINASFINGYQEKNFIAAQPKKEETVNDWRMIWEQNTATIVMVT 340
2 (V) 331
1 NLKERKECKAQYWPQGCWTYGNIRSVSEDTVLVDYTVRKFCIQQVQDMTNRKPQRLITQFHFTSW 408
2 V S V 399
1 PDFGVPFTPIGMLKFLKKVKACNPQYAGAI VHCAGVGRGTGFVIDAMLDMHTERKVDVYGVFSR 476
2 S 467
1 IRAQRQCMVQTDNQYFYIYQALLEHYLYGDTLEVTSLETHLQIYNKIPGTSNNGLEEEFKKLTSIK 544
2 535
1 IQNDKMRITGNLPANMKKNRVLQIIPYEFNRV IIPVKRGEENTIDYVNASFIDGYRQKDSYIASQGPLLH 612
2 (VII) 603
1 TIEDFWRM IWEWKSCSIVMLTELEERGQEKCAQWPQSDGLVSYGDI TVELKKEECECYTVRDLLVTN 680
2 671
1 TRENKSRQIRQFHFGWPEVGIPSDGKGMISIIAAVQKQQQSGNHPITVHCAGAGRTGTCALSTV 748
2 N 739
1 LERVKAEGILDVFQTVKSLRLQRPHMVQTLQEQEFCYKVVOEYIDAFSDYANFK 802
2 793

FIG. 4D

	10	20	30	40	
LCA	NqnKNRYVdILPYDynRVeL	sEinGdagSnYINASyIdGf	kEprKyIAA		
RPTase α	NKeKNRYVNILPYDHSRVhLtpvE	GvpdSDYINASfInGYqEknKfIAA			
RPTase β	NKHKNRYINIVAYDHSRVKL	aqLaekDgKItDYINANYVDGYNrpKAYIAA			
RPTase γ	NKHKNRYINIIAYDHSRVKL	rpLpgKDskhsDYINANYVDGYNkaKAYIAA			
CON	NkhKNRY-nII-YDhsRVkL	—l—k—k—sdYINA—y—dGyne	pk—yIAa		
	50	60	70	80	90
LCA	QGPrdETVdDFWRMIWEQ	katvIVMVT	rceEgnrnKCAeYWP	sMeegTra	
RPTase α	QGPkeETVnDFWRMIWEQ	NlatIVMVTNL	kErkeckCAQYWP	dqGewTYG	
RPTase β	QGPLKSTaEDFWRMIWEhN	vevIVMITNL	VEKGRRKCDQYWP	adGSEEYg	
RPTase γ	QGPLKSTfEDFWRMIWEqN	lgiIVMITNL	VEKGRRKCDQYWP	tenSEEYg	
CON	QGPIk-TveDFWRMIWEqnt-vIVM-TnlvEkgr	rkC-qYWP—gse-yg			
	100	110	120	130	
LCA	fgdVvVkinqhkr	cpDYiiqKI	nIvn	kkekatgRevThiq	
RPTase α	NirVsVedVtVLv	DYTVRKFc	IqqvGd	mtnRkpqRIiTQfH	
RPTase β	NfIVTqKSVqVLA	yYTVRnftIRNTKIKK	Gs	qKGRpsgRVVTQYH	
RPTase γ	NiiVTIKStkihAc	YTVRrFsiRNTKvKK	GqkgnpKGRqneRVViQYH		
CON	ni-Vlvk-v-vla—dYlv	rkf—rntki—k—g—k—kgr—qRvvtqyh			

FIG.5A

	140	150	160	170	180	190
LCA	FTSWPDhGVPedPhIILKlrrrrVnAfsnffsGpIVVHCSAGVGRTGTyigID					
RPTase α	FTSWPDfGVPftPigmLKfIkKVkAcnpqyaGaIVVHCSAGVGRTGTfvVID					
RPTase β	YTQWPDmGVPEYsLPVLTfVRKaaYAkRhavGPVVVHCSAGVGRTGTyIVID					
RPTase γ	YTQWPDmGVPEYaLPVLTfVRrssaArmpetGPVIVHCSAGVGRTGTyIViD					
CON	-T-WPDmGVPeypIplvL-fvr-v-aa-Gp-vVHCSAGVGRTGTyiviD					

	200	210	220	230
LCA	AMLegleaEnKVDVYGyVvkIRrQRCIMVQveaQYiIHQALvE			
RPTase α	AMLdmmhtErKVDVYGFVsrIRaQRCqMVQTdmQYVFlyQALIE			
RPTase β	SMLQQIqhEgTVNiFGFLKHIRsQRNYLVQTEEQYVFIDHLLvE			
RPTase γ	SMLQQIkdkSTVNvIGFLKHIRtQRNYLVQTEEQYIFIDaLIE			
CON	-MLqqi-e-V-vyGf-khIR-QR-y-VQteeQY-fIH-aL-E			

FIG.5B

	10	20	30	40
LCA	NksKNRnsnvIPYdyNRVp	lkhelemskesehdssdessdddsds	EEpskY	
RPTase α	NmkKNRvIqIIPYEfNRVi	lpvkr	GEE	nTDY
RPTase β	NrEKNRLSSIPvERsRVG	lsslS	GE	GTDY
RPTase γ	NkEKNRnSSvvPsERaRVG	lapLp	Gmk	GTDY
CON	NkeKNRnss-iPyernRVg	l	geegt	dY
	50	60	70	80
LCA	iNASFImSYwkpevmI	AoQGPLkeTlgDFWqMI	fqrKvkvIVMLTEL	khg
RPTase α	vNASFIdGYrQkdsyI	AsQGPLLHTleDFWRMI	WewKscsIVMLTE	leer
RPTase β	INASYIMGYYSNEF	ITQHPLLHTIKDFWRMI	WOHNAQIVVMiPDgQnm	
RPTase γ	INASYIMGYYSNEF	ITQHPLpHTIKDFWRMI	WOHNAQiiVMiPDnQsI	
CON	iNAS-ImgYyqsnefI	-tQ-PLIhTikDFWrMI	wdh-naqiVMI	—q—
	100	110	120	130
LCA	dQEiCAQYW	geGkqtYGDleVdLKdtdksstYTl	RvfeIrhskrk	dSRltv
RPTase α	gQEiCAQYWPsdG	lvsYGDItVeLKkeeeCESYTV	RdIlvtntreNkSRqI	
RPTase β	A EDEFVYWPn	kDEpi	NCESFkVTLmaeehkCLSNEEkiI	
RPTase γ	A EDEFVYWPs	reEsm	NCEaFtVTLiskdrICLSNEEqiI	
CON	aE-e-qYWps-g	—ygd—v-lk—nces-lvt—e-r-clsne-r-i		
	150	160	170	180
LCA	yQy	qY tnWsvEqIP	aepKellSmIqvVkkQKlpQk	
RPTase α	rQf	HF hgWPevgiP	SdgKgmISilaaV Qk Qq	
RPTase β	IQDFILEATQDDYVLEVRHF	QCPKWPNDsPISkTFELISVI		K
RPTase γ	IhDFILEATQDDYVLEVRHF	QCPKWPNDaPISsTFELInVI		K
CON	iqdfileatqddyvlevrhf	qcpkwpnpd-Pis-t-ellsvI	—qk	

FIG.5C

	190	200	210	220	230
LCA	nsseGNkhhkstP	IIiHCrdGsqqTG	iFCALIniLEsaetE	evvDiFQvVKa	
RPTase α	qqsGNh	PitVHCsaGagr	TGTFCALsTvLE	ervkaEgiIDVFQt	VKs
RPTase β	EEAaNR	DGPmIVHDEhGgVt	AGTFCALTTLmhQLE	kENsVDVyQVAKM	
RPTase γ	EEAItR	DGPtIVHDEyGaVs	AGmICALTTLsqQLE	ENaVDVfQVAKM	
CON	-eea-nr---	dgP-ivH-e-Gav-	GtfCALtllleqle-	En-vDvfQv-Km	

	240	250
LCA	LrkaRPgMVSTfEQYqFIYd	Vias
RPTase α	LaLqRPhMVqTIEQYefcYKVvqe	
RPTase β	INLMRPGVFtDIEQYQFIYKVILS	
RPTase γ	INLMRPGVFtDIEQYQFIYKArLS	
CON	-nlmRPg---	iEQYqFIYkvils

FIG.5D

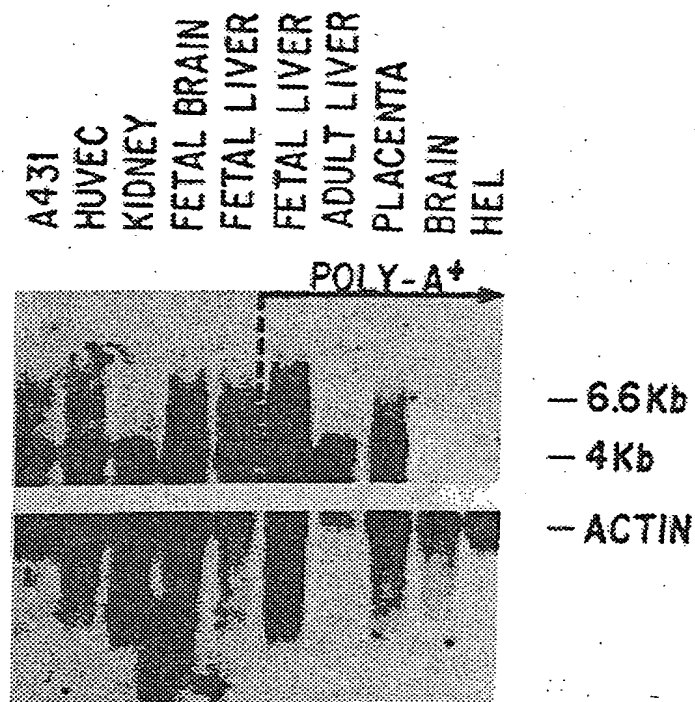
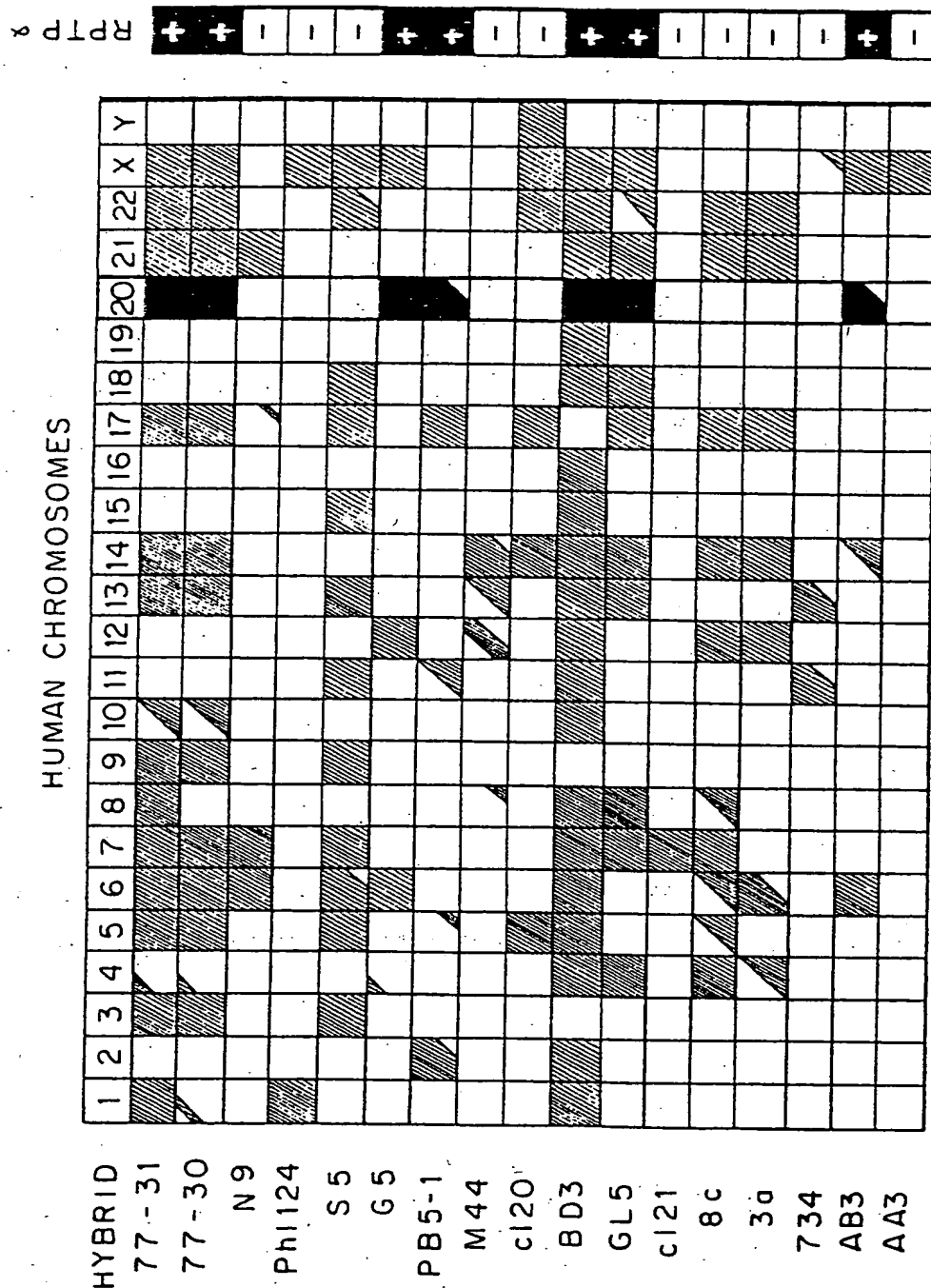


FIG. 6

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FIG. 7

HUMAN CHROMOSOMES



1 ATGGATTCTGGTTCATTCTTGTCTGCTCGGCAGTGGTCTGATATGTGTCAGTGCCAAC 60
1 [M D S W F I L V L L G S G L I C V S] A N 20
SIGNAL PEPTIDE

61 AATGCTACCACAGTTGCACCTTCTGTAGGAATTACAAGATTAACTCATCAACCGCA 120
21 N A T T V A P S V G I T R L I N S S T A 40

121 GAACCAAGTTAAAGAAGAGGCCAAAACCTCAAATCCAACTTCTTCACTAACTTCTCTTTCT 180
41 E P V K E E A K T S N P T S S L T S L S 60

181 GTGGCACCACATTTCAGCCCAAATATAACTCTGGGACCCACCTATTTAACCCTGTCAAT 240
61 V A P T F S P N I T L G P T Y L T T V N 80

241 TCTTCAGACTCTGACAATGGGACCACAAGAACAGCAAGCACCAATTCTATAGGCATTACA 300
81 S S D S D N G T T R T A S T N S I G I T 100

301 ATTTACCAAATGGAACGTGGCTTCCAGATAACCAGTTCACGGATGCCAGAACAGAACCC 360
101 I S P N G T W L P D N Q F T D A R T E P 120

361 TGGGAGGGGAATTCCAGCACCGCAGCAACCACTCCAGAACTTTCCCTCCTTCAGGTAAT 420
121 W E G N S S T A A T T P E T F P P S G N 140

421 TCTGACTCGAAGGACAGAAGAGATGAGACACCAATTATTGCGGTGATGGTGGCCCTGTCC 480
141 S D S K D R R D E T [P I I A V M V A L S 160
TRANSMEMBRANE SEGMENT

481 TCTCTGCTAGTGATCGTGTTTATTATCATAGTTTGTACATGTTAAGGTTTAAGAAATAC 540
161 S L L V I V F I I I V L Y M L] R F K K Y 180

541 AAGCAAGCTGGGAGCCATTCCAATTCTTTCCGCTTATCCAACGGCCGCACTGAGGATGTG 600
181 K Q A G S H S N S F R L S N G R T E D V 200

601 GAGCCCCAGAGTGTGCCACTTCTGGCCAGATCCCCAAGCACCAACAGGAAATACCCACCC 660
201 E P Q S V P L L A R S P S T N R K Y P P 220

661 CTGCCCCGTGGACAAGCTGGAAGAGGAAATTAACCGGAGAATGCCAGACGACAATAAGCTC 720
221 L P V D K L E E E I N R R M A D D N K L 240

721 TTCAGGGAGGAATTCAACGCTCTCCCTGCATGTCCTATCCAGGCCACCTGTGAGGCTGCT 780
241 F R E E F N A L P A C P I Q A T C E A A 260

781 TCCAAGGAGGAAAAACAAGGAAAAAATCGATATGTAAACATCTTGCCTTATGACCACTCT 840
261 S K E E [N K E K N R Y V N I L P Y D H S 280
PTPase DOMAIN I

FIG.8A

841 AGAGTCCACCTGACACCGGTTGAAGGGTTCCAGATTCTGATTACATCAATGCTTCATTC 900
281 R V H L T P V E G V P D S D Y I N A S F 300

901 ATCAACGGTTACCAAGAAAAGAACAAATTCATTGCTGCCACAAGGACCAAAGAAGAAACG 960
301 I N G Y Q E K N K F I A A Q G P K E E T 320

961 GTGAATGATTTCTGGCGGATGATCTGGGAACAAAACACAGCCACCATCGTCATGGTTACC 1020
321 V N D F W R M I W E Q N T A T I V M V T 340

1021 AACCTGAAGGAGAGAAAGGAGTGCAAGTGGCCCCAGTACTGGCCAGACCAAGGCTGCTGG 1080
341 N L K E R K E C K C A Q Y W P D Q G C W 360

1081 ACCTATGGGAATATTCGGGTGTCTGTAGAGGATGTGACTGTCTCTGGTGGACTACACAGTA 1140
361 T Y G N I R V S V E D V T V L V D Y T V 380

1141 CGGAAGTTCTGCATCCAGCAGGTGGGCGACATGACCAACAGAAAGCCACAGCGCCTCATC 1200
381 R K F C I Q Q V G D M T N R K P Q R L I 400

1201 ACTCAGTTCCACTTTACCAGCTGGCCAGACTTTGGGGTGCCTTTTACCCGATCGGCATG 1260
401 T Q F H F T S W P D F G V P F T P I G M 420

1261 CTCAAGTTCCTCAAGAAGGTGAAGGCCTGTAACCCTCAGTATGCAGGGGCCATCGTGGTC 1320
421 L K F L K K V K A C N P Q Y A G A I V V 440

1321 CACTGCAGTGCAGGTGTAGGGCGTACAGGTACCTTTGTCGTCATTGATGCCATGCTGGAC 1380
441 H C S A G V G R T G T F V V I D A M L D 460

1381 ATGATGCATACAGAACGGAAGGTGGACGTGTATGGCTTTGTGAGCCGGATCCGGGCACAG 1440
461 M M H T E R K V D V Y G F V S R I R A Q 480

1441 CGCTGCCAGATGGTGCAAACCGATATGCAGTATGTCTTCATATACCAAGCCCTTCTGGAG 1500
481 R C Q M V Q T D M Q Y V F I Y Q A L L E] 500

1501 CATTATCTCTATGGAGATACAGAACTGGAAGTGACCTCTCTAGAAACCCACCTGCAGAAA 1560
501 H Y L Y G D T E L E V T S L E T H L Q K 520

1561 ATTTACAACAAAATCCCAGGGACCAGCAACAATGGATTAGAGGAGGAGTTTAAGAAGTTA 1620
521 I Y N K I P G T S N N G L E E E F K K L 540

FIG.8B

1621 ACATCAATCAAAATCCAGAATGACAAGATGCGGACTGGAAACCTTCCAGCCAACATGAAG 1680
541 T S I K I Q N D K M R T G N L P A [N M K 560
PTPase Domain II

1681 AAGAACCGTGTTTTACAGATCATTCCATATGAATTCAACAGAGTGATCATTCCAGTTAAG 1740
561 K N R V L Q I I P Y E F N R V I I P V K 580

1741 CGGGGCGAAGAGAATACAGACTATGTGAACGCATCCTTTATTGATGGCTACCGGCAGAAG 1800
581 R G E E N T D Y V N A S F I D G Y R Q K 600

1801 GACTCCTATATCGCCAGCCAGGGCCCTCTTCTCCACACAATTGAGGACTTCTGGCGAATG 1860
601 D S Y I A S Q G P L L H T I E D F W R M 620

1861 ATCTGGGAGTGGAATCCTGCTCTATCGTGATGCTAACAGAACTGGAGGAGAGAGGCCAG 1920
621 I W E W K S C S I V M L T E L E E R G Q 640

1921 GAGAAGTGTGCCCAGTACTGGCCATCTGATGGACTGGTGTCTATGGAGATATTACAGTG 1980
641 E K C A Q Y W P S D G L V S Y G D I T V 660

1981 GAACTGAAGAAGGAGGAGGAATGTGAGAGCTACACCGTCCGAGACCTCCTGGTCACCAAC 2040
661 E L K K E E E C E S Y T V R D L L V T N 680

2041 ACCAGGGAGAATAAGAGCCGGCAGATCCGGCAGTTCCACTTCCATGGCTGGCCTGAAGTG 2100
681 T R E N K S R Q I R Q F H F H G W P E V 700

2101 GGCATCCCCAGTGACGGAAGGGCATGATCAGCATCATCGCCGCCGTGCAGAAGCAGCAG 2160
701 G I P S D G K G M I S I I A A V Q K Q Q 720

2161 CAGCAGTCAGGGAACCCACCCATCACCGTGCAGCGCCGGGGCAGGAAGGACGGGG 2220
721 Q Q S G N H P I T V H C S A G A G R T G 740

2221 ACCTTCTGTGCCCTGAGCACCGTCTGGAGCGTGTGAAAGCAGAGGGGATTTTGGATGTC 2280
741 T F C A L S T V L E R V K A E G I L D V 760

2281 TTCCAGACTGTCAAGAGCCTGCGGCTACAGAGGCCACACATGGTCCAGACACTGGAACAG 2340
761 F Q T V K S L R L Q R P H M V Q T L E Q 780

2341 TATGAGTTCTGCTACAAGGTGGTGCAGGAGTATATTGATGCATTCTCAGATTATGCCAAC 2400
781 Y E F C Y K V V Q E] Y I D A F S D Y A N 800

2401 TTCAAGTAA 2409
801 F K * 803

FIG.8C